

**IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF MARYLAND**

THE UNITED STATES OF AMERICA

v.

EARL WHITTLEY DAVIS

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* Criminal Case No. RWT 07-0199
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MEMORANDUM OPINION

Defendant Earl Whittley Davis has been indicted for federal crimes relating to the robbery and murder of Jason Schwinder on August 4, 2004, and the Government has given notice of its intent to seek the death penalty. Trial is now set to begin on March 31, 2009.

The Defendant has filed a Motion to Exclude DNA Test Results and Request for *Daubert* Hearing [Paper No. 42], which seeks to preclude the Government from introducing at trial certain items and opinions relating to DNA evidence. Although Defendant raises a myriad of objections, two issues predominate the pleadings on this issue. The first is whether the DNA evidence in this case should be excluded under a *Daubert* analysis because low copy number (LCN) testing allegedly was utilized, and this type of testing is a new methodology (“the latest fad”) that is not sufficiently reliable. The second is whether the disagreement in the scientific community as to the best method of explaining the statistical significance of a “cold hit” DNA database match should preclude the introduction of the DNA evidence flowing from a cold hit.

PROCEDURAL HISTORY

Defendant was arrested in October 2004 and was initially prosecuted in the Circuit Court for Prince George’s County. On the eve of the state trial set for April 2007, the state charges were dismissed by the State’s Attorney for Prince George’s County and the federal prosecution

commenced with the filing of a criminal complaint. On April 30, 2007, a federal grand jury returned a six-count indictment alleging a Hobbs Act robbery, carjacking, and related firearms violations. The death-eligible offense is murder by use of a firearm in furtherance of a Hobbs Act robbery in violation of 18 U.S.C. § 924(j).

On March 7, 2008, counsel for the Government received notice that the Attorney General had authorized the United States Attorney for the District of Maryland to seek a death sentence in this case. The Government informed the Court of this authorization on March 10, 2008.

On March 31, 2008, the grand jury returned a superseding indictment for the same offenses that added the death-qualifying intent elements and statutory aggravating factors. On April 8, the Government filed formal notice of intent to seek the death penalty [Paper No. 40].

On April 4, 2008, the Defendant filed the instant Motion to Exclude DNA Test Results and Request for *Daubert* Hearing [Paper No. 42] (hereinafter, “Def. Mot.”). The Government filed its Consolidated Response to Defendant’s Pretrial Motions on July 15, 2008 [Paper No. 92] (hereinafter, “Resp.”). The Defendant filed his Reply [Paper No. 124] (hereinafter, “Reply”) on August 21, 2008, but at this point the Government had not filed any affidavits in support of its Response.

On August 22, 2008, the Government filed the affidavit of Meredith Kitey, the former DNA Laboratory Manager, Technical Leader and CODIS¹ Administrator for the Prince George’s Police Department, in support of its Response [Paper No. 135-2] (hereinafter, “Kitey Aff. I”). The

¹ CODIS refers to the Combined DNA Index System, which is an automated DNA information processing and telecommunications system that supports the National DNA Index System (NDIS), State DNA Index (SDIS), and local DNA Index (LDIS). CODIS contains DNA profiles from convicted offenders and crime scene evidence and is used as an investigative tool to identify suspects by comparing DNA profiles. See <http://www.fbi.gov/hq/lab/html/codis1.htm> (last visited February 9, 2009).

Defendant filed a Supplemental Reply [Paper No. 154] on September 22, which includes three lengthy affidavits from experts refuting the contentions of the Government's expert. The Government then filed a Supplemental Affidavit of Ms. Kitey on October 6 [Paper No. 155-2](hereinafter, "Kitey Aff. II").

The Court held a hearing on the Defendant's other pretrial motions on September 15, 2008, but deferred the hearing of the instant motion until October 10, 2008. As explained below, the motion will be denied.

FACTUAL BACKGROUND

On August 6, 2004, shortly before 1:00 p.m., Jason Schwindler, an armored car employee, picked up a bank deposit from a local business and took it to a nearby BB&T bank in Hyattsville, Maryland. Schwindler got out of the armored car, and as he walked up to the bank entrance, two gunman exited a Jeep Cherokee and began shooting at Schwindler, killing him. When their escape in the Jeep was thwarted by the armored truck driver, the assailants carjacked a bank customer and fled in her vehicle. The carjacked vehicle was later recovered.

After the murder, officers from the Prince George's County Police Department responded to the crime scene and collected evidence. Numerous items were recovered, including a baseball cap worn by one of the shooters, two firearms, and steering wheel covers from the Jeep Cherokee and a Pontiac Grand Am that were used by the suspects in the commission of the offense. These items were swabbed and analyzed for DNA. The DNA profiles of the major contributor to the DNA found in the ball cap and on the trigger and grip of the recovered firearms were entered into the local CODIS database. As a result of a search of the local database, on or about August 14, 2004, there was a "hit" between the DNA recovered from the

ball cap recovered at scene and the DNA of the Defendant. Law enforcement officers were notified of the match and advised to obtain a known sample from the Defendant. Pursuant to a search warrant, a DNA sample was taken from him and compared to the items recovered from the crime scene.

The DNA analysis was performed by the Prince George's County Serology/DNA Laboratory. The lab utilized a method of testing known as PCR/STR² typing to analyze the DNA in this case. Each laboratory report notes: "DNA isolated from the indicated items was amplified using the PCR and typed for the STR loci D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX, CSF1PO, and for gender (X,Y) using the AmpFister Profiler Plus™ and COFiler™ PCR Amplification kits." (Def. Mot. Ex. 1, Results of Forensic Examination (March 5, 2007)). The results included the following:

Ballcap (N6)

As previously reported, DNA from more than one individual was obtained from the ballcap (N6). The major component of the profile matches the known profile of Earl Davis (DS1). To a reasonable degree of scientific certainty, in the absence of an identical twin, Earl Davis is the source of this DNA. The minor types remain unassigned. Opio Moore (A), Kwang Yeung Yan (MS1), Kathryn Hollins (KH), and Robert Sineway (RS) are excluded as potential contributors.

Trigger & grip of Glock model 22 handgun (N1b)

As previously reported, DNA from more than one person was obtained from the swabbing of this item. This is a partial profile, which may be due to degraded and/or an insufficient quantity of DNA. Several of the types in this profile are consistent with the known profile of Earl Davis (DS1). Several of the types in this profile are also consistent with the known profile of Opio Moore (A). However, due to the limited nature of this profile, no statistical calculations can be performed. Kwang Yeung Yan (MS1), Kathryn Hollins (KH), and Robert Sineway (RS) are excluded as potential contributors. No further conclusions can be made regarding this profile.

² PCR/STR typing is discussed *infra*, Section I.A.(2).

Trigger & grip of Taurus model PT-92AF handgun (N2d)

As previously reported, DNA from more than one person was obtained from the swabbing of this item. This partial profile, which may be due to degraded and/or an insufficient quantity of DNA. Several of the types in this profile are consistent with the known profile of Opio Moore (A). However, there are additional types present that are unassigned at this time. Due to the limited nature of this profile, no statistical calculations can be performed. Earl Davis (DS1), Kwang Yeung Yan (MS1), Kathryn Hollins (KH), and Robert Sineway (RS) are excluded as potential contributors. No further conclusions can be made regarding this profile.

Jeep Cherokee steering wheel (BG1)

As previously reported, DNA from more than one individual was obtained from the steering wheel of the Jeep Cherokee (BG1). This profile is consistent with the combined profiles of Kwang Yeung Yan (MS1) and Earl Davis (DS1). The DNA profile obtained from this item is approximately:

- 3.5 quadrillion times more likely to be a mixture of DNA from Kwang Yeung Yan and Earl Davis than a mixture of Kwang Yeung Yan and an unknown individual in the Caucasian population.
- 510 billion times more likely to be a mixture of Kwang Yeung Yan and Earl Davis than a mixture of Kwang Yeung Yan and an unknown individual in the African-American population.
- 4.3 quadrillion times more likely to be a mixture of DNA from Kwang Yeung Yan and Earl Davis than a mixture of Kwang Yeung Yan and an unknown individual in the southeast Hispanic population.

Opio Moore (A), Kathryn Hollins (KH), and Robert Sineway (RS) are excluded as possible contributors.

Pontiac Grand Am steering wheel (K3)

As previously reported, DNA from more than one individual was obtained from the steering wheel of the Pontiac Grand Am (K3). The major component of the profile matches the known profile of Earl Davis (DS1). To a reasonable degree of scientific certainty, in the absence of an identical twin, Earl Davis is the source of this DNA. The minor types are consistent with the known profile of Kathryn Hollins (KH). Opio Moore (A), Kwang Yeung Yan (MS1), and Robert Sineway (RS) are excluded as possible contributors.

DNA from more than one individual was obtained from the Grand Am shifter (K1C). Earl Davis and Kathryn Hollins cannot be excluded as possible contributors to this mixture. Kwang Yeung Yan, Opio Moore, and Robert Sineway are excluded as potential contributors.

The items listed above were not fully consumed during the course of analysis.

Additional portions are available for independent testing.

(Def. Mot. Ex. 1, Results of Forensic Examination (Dec. 6, 2004)) (internal footnotes omitted).

The Defendant challenges the admissibility of this DNA evidence on a number of grounds.

LEGAL STANDARDS

The admissibility of expert testimony is governed by Federal Rule of Evidence 702, which states:

If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if (1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the witness has applied the principles and methods reliably to the facts of the case.

The Court must also be mindful of Rule 403, which provides that

Although relevant, evidence may be excluded if its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by considerations of undue delay, waste of time, or needless presentation of cumulative evidence.

The Supreme Court's decision in *Daubert v. Merrill Dow Pharmaceuticals*, 509 U.S. 579 (1993), requires that trial courts make a "preliminary assessment" of whether proffered expert testimony is both reliable ("based on scientific knowledge") and helpful ("of assistance to the trier of fact in understanding or determining a fact in issue"). See *Maryland Casualty Co. v. Therm-O-Disc, Inc.*, 137 F.3d 780, 783 (4th Cir. 1998). "The *Daubert* court described this mandated inquiry as 'a preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology

properly can be applied to the facts in issue.” *Id.* at 784.

The *Daubert* opinion listed a set of four factors that the court should consider when making such evaluations, but these factors are not “a definitive checklist or test,” and no single factor is determinative. 509 U.S. at 593. These factors are: (1) whether the proposed technique used by the expert can be, and has been, tested; (2) whether the theory or technique has been subjected to peer review and publication; (3) the known or potential rate of error of the method used; and (4) the degree of the method’s or conclusion’s acceptance within the relevant scientific community. *Id.* at 593-95.

It is clear that a court is not required to hold a hearing simply because a party has raised a *Daubert* issue.

Beyond establishing the two criteria of reliability and helpfulness, the Court has left the means by which these criteria are evaluated to the sound discretion of the district judge. This is apparent not only from *Daubert* itself, but from subsequent Supreme Court precedent, holding that abuse of discretion is the proper standard by which evaluations of proffered evidence should be reviewed. In addition, this circuit has taken the position that the *Daubert* court “was not formulating a rigid test or checklist,” and was “relying instead on the ability of federal judges to properly determine admissibility.”

Therm-O-Disc, 137 F.3d at 785 (internal citations omitted).

In this case, the briefing and affidavits on this motion are extensive. The Court held a hearing on October 10, 2008, solely to resolve some underlying factual disputes (see *infra*). As explained below, the Court concludes that no *Daubert* hearing is necessary, and will proceed to address each of the points made in the motion.

ANALYSIS

I. FORENSIC DNA TESTING³

A. Description of Basic DNA Testing

1. Basic Chemistry⁴

Each human body contains a large number of cells, each of which descends from successive divisions of the fertilized egg that was its origin. Virtually all non-reproductive cells in the body contain identical copies of a complex structure called deoxyribonucleic acid, or DNA. This structure represents the genetic code for that individual. The DNA is in the form of microscopic chromosomes, which are located in the nucleus of a cell. A chromosome is a thread of DNA surrounded by other materials, mainly protein. A fertilized egg contains 23 chromosomes, with one member of each pair being contributed by the mother and father, respectively. Each cell contains exact duplicates of the 46 cells from the fertilized parent cell. Therefore, each cell in the human body has the same DNA.

The structure of DNA consists of two strands, coiled in the form of a double helix, i.e., a twisted ladder. Each strand is composed of a string or a sequence of nucleotide bases held together by a sugar-phosphate backbone. To use the ladder metaphor, running between the sugar-phosphate strands (the side rails of the ladder) are billions of rungs, each of which is

³ Much of the Court's scientific discussion in this section is taken almost verbatim from Judge Sleet's excellent opinion in *United States v. Trala*, 162 F. Supp. 2d 336 (D. Del. 2001).

⁴This description of the basic concepts of DNA is derived from National Research Council, *The Evaluation of Forensic DNA Evidence* 12-14, 60-65 (1996) [hereinafter, "NRC II"]. The NRC II is widely regarded as one of the definitive publications on the use of DNA evidence in the field of forensics. See also, e.g., *United States v. Gaines*, 979 F. Supp. 1429, 1431-32 (S.D.Fla.1997) (citing *United States v. Shea*, 957 F. Supp. 331, 333 (D.N.H.1997)); *Government of Virgin Islands v. Penn*, 838 F. Supp. 1054, 1058 (D.Vi.1993).

composed of two bases. There are only four possible types of bases—A, T, G, C, which represent adenine, thymine, guanine, and cytosine, respectively. The order in which the base pairs appear on the DNA ladder constitutes an individual's genetic code.

A gene is a particular DNA sequence located along a chromosome, ranging from a few thousand to tens of thousands of base pairs, that produces a specific product in the body. In other words, a gene is a site (a sequence of letters) on the DNA that encodes for a protein. A marker is a site on the DNA that does not code for proteins; the marker is also known as the locus (or location, plural "loci"). In essence, the specific base sequence on the gene acts as an encoded message to the body to produce certain amino acids, which ultimately combine to form a protein. The function of a given gene is determined by the order of bases in the gene. The position that gene occupies along the DNA thread is known as its locus.

Human beings share more biological similarities than differences. Thus, over 99% of human DNA does not vary from person to person. Each person's DNA, however, has certain regions where the rungs of the ladder will be different. These areas where loci are different are called "polymorphic" regions. The possible arrangements of base pairs that could occur in one of these polymorphic areas (i.e., the alternative forms of a gene that an individual could possess) are known as alleles. These alleles can result from differences in single base pairs, differences in multiple base pairs, or differences in the number of base pairs found in a given region. The individual genetic makeup described by the alleles is known as the genotype. In forensic analysis, the genotype for a group of analyzed loci is called the DNA profile. When a sample of DNA is typed, the lab examiner looks at predetermined polymorphic loci, identifies the alleles that make up the DNA sequence at those polymorphic loci, and then determines how likely it is

for this sequence to appear in a given population.

2. Description of DNA testing

In this case, the laboratory used a method of DNA typing known as PCR/STR typing. In PCR/STR typing, a process known as polymerase chain reaction, or PCR, is used to amplify targeted loci of the sample of DNA by replicating the process by which DNA duplicates itself naturally. Thus, the lab is able to produce a substantial number of specific, targeted segments of DNA which can then be typed and compared. Short Tandem Repeats, or STR's, are a group of loci which are used to type and compare the DNA. Finally, statistics are used to evaluate how likely it is that a similar match would occur if the DNA sample were drawn randomly from the population. The Court will briefly further describe the typing methods used below.

a. PCR Amplification Process⁵

PCR, a sample preparation technique, is a laboratory process for copying a short segment of DNA millions of times. The PCR process is analogous to the process by which cells replicate their DNA naturally. *See United States v. Gaines*, 979 F. Supp. 1429, 1435 (S.D. Fla. 1997). By using this process, a lab can produce a substantial number of specific, targeted segments of DNA which can then be typed and compared. PCR allows the laboratory to amplify only those specific DNA regions which exhibit genetic variations within the population, allowing for DNA typing. Moreover, the PCR process enables the analysis of very tiny amounts of DNA. PCR also

⁵*See generally*, NRC II, at 69-71. *See also United States v. Beasley*, 102 F.3d 1440, 1445 (8th Cir.1996); *United States v. Hicks*, 103 F.3d 837, 844-45 (9th Cir.1996); *Shea*, 957 F. Supp. at 334.

permits the analysis of old and/or degraded DNA samples.

The PCR process is comprised of three steps. First, the double-stranded segment of DNA is separated, or denatured, into two strands by heating. This denatured DNA strand forms a template that can allow the manufacture of a new strand that is identical to its former complementary strand.

Next, each of the single-strand segments is hybridized with primers. Primers are short DNA segments that are designed to bind with the template at particular loci. The primers are designed to complement a sequence just outside of a target sequence of bases.

Finally, each primer serves as a starting point for the replication of the target sequence. In this third step, a type of enzyme called a polymerase becomes active. In essence, the polymerase facilitates repeated additions of bases to the primer until a new, complimentary strand of the targeted DNA locus is created.

This process is repeated a number of times, creating an exponentially increasing number of copies of the targeted area of the original DNA. Eventually, the PCR amplification process yields a sufficient quantity of the DNA sample to be typed. If the laboratory wants to type the DNA sample at multiple sites, it can add additional primers which will bind simultaneously to their respective target sites. This process is known as multiplexing. Multiplexing allows the laboratory to minimize the chance of human error and contamination in the PCR process. Using current technology, the FBI laboratory can multiplex up to fifteen or sixteen markers with reliable results.

b. Short Tandem Repeats⁶

The PCR process is performed to amplify a targeted locus (or loci) for analysis. These loci are selected because they are polymorphic, thus making them amenable to typing. One group of such loci involve a class of repeated units, distributed widely throughout the DNA structure, known as short tandem repeats (“STR’s”). A tandem repeat involves multiple copies of an identical DNA sequence arranged in direct succession in a particular region of a chromosome. An STR is a tandem repeat in which the core repeat units are just a few base pairs. Loci containing STR’s are scattered throughout the chromosomes in enormous numbers. Such loci have a fairly large number of alleles and are usually capable of unique identification. See *Commonwealth v. Rosier*, 685 N.E.2d 739, 742 (Mass. 1997).

Once the amount of DNA is amplified by the PCR process, the analyst proceeds to identify fragments of different sizes by their migration in an electric field. In order to detect variations, analysts use a process known as electrophoresis. During the PCR amplification of the STR fragments, the primers that are used contain fluorescent tags, which become incorporated into the STR fragments during amplification. During electrophoresis, the amplified fragments will pass through a gel and eventually pass through a detection window at the end of the gel. The fragments can be passed through either a flat slab gel or through a small-diameter capillary that contains a gel or liquid polymer. The difference between these two methods is that the flat gel permits multiple samples to be run at the same time, while capillary electrophoresis only permits one sample to be run at a time. The scientific principles underlying both techniques are the same.

After the fragments pass through the detection window at the end of the gel, a laser fires,

⁶See generally *Commonwealth v. Rosier*, 685 N.E.2d 739 (Mass. 1997)

striking the fluorescent tags, and causing the tags to emit light. A camera will detect the light and convert it into data. By measuring the amount of time that it takes a particular fragment to reach the laser, the laboratory will be able to determine the size of the fragment and, therefore, it will be able to determine the number of sequence repeats. The faster a fragment moves through the window, the smaller it is in size and vice versa.

The data generated are analyzed by an accompanying computer software program which determines the size of the alleles based on the rate at which they reach the window. The software detects the light being emitted and converts it into peaks of different sizes. The analyst then compares the configuration of these peaks against known reference standards in order to determine the number of alleles present at the target loci in a given sample. The signal must be of a certain strength, that is, the peak must be high enough to be interpreted before a laboratory will have enough confidence in the data to make an interpretation.

c. Cofiler and Profiler Kits

In this case, the PCR process was used to amplify thirteen STR loci. The thirteen STR's typed in this case are the core DNA markers used in the development of the Combined DNA Index System, or CODIS.⁷ CODIS is a national database containing DNA profiles of convicted felons. In order to amplify the DNA samples at these particular loci, the laboratory used two kits that contain the materials necessary to accomplish this result. These kits are known as the

⁷All of the samples in the CODIS data bank are typed at the same thirteen STR loci, thus enabling law enforcement to compare unknown samples with samples in the data bank. CODIS was developed by a consortium of twenty-one laboratories to test various STR markers to determine which would be the best to use in the CODIS data bank. The thirteen used in this case were selected for CODIS and are, therefore, known as the CODIS core loci.

Profiler Plus and Cofiler DNA Typing Systems and are manufactured by Perkin Elmer Applied Biosystems.

These kits contain three basic materials: primers, reaction mix and polymerase. The kits also contain the fluorescent tags that allow the amplified DNA fragments to be detected during the electrophoresis phase. The reaction mix is a combination of chemicals used in any form of PCR testing that, in essence, creates the proper chemical environment for the PCR process to occur. The reaction mix is not locus-specific. The polymerase is a class of enzymes that enable bases to be added to the primer. It too, is not locus-specific.

The elements of the kits that are locus-specific are the primers. The primers are small fragments of DNA designed to bind with particular loci when the two strands of the DNA sample are separated. These primers do not represent new methods of performing PCR, or even modifications of the PCR process. The primers are simply known sequences of DNA bases which have been identified as occurring in every human on the boundary of the locus to be tested.

3. Statistical Methodology⁸

Once two DNA samples (i.e., the defendant's DNA and what was found on the evidence) are typed at a number of STR loci and are found to be sufficiently similar such that they could have originated from the same source, the analyst must determine the significance of the comparison. In other words, the analyst must determine how common or rare the particular DNA profile is based on population frequency data. The analyst does this by calculating the profile

⁸See *Shea*, 957 F. Supp. at 335-37.

frequency, also called the random match probability. The profile frequency is simply the probability that an unrelated person chosen at random from the population would have the same DNA profile as the unknown sample.

The analyst will determine the statistical frequency of a particular DNA profile by multiplying the frequency of each of the alleles in the profile, and then correcting the result to account for inbreeding⁹ or substructuring¹⁰ effects in the population. In other words, the statistical frequency of the DNA profile is calculated using a statistical concept known as the product rule.

B. Low Copy Number Testing

The Defendant moves for exclusion of DNA evidence and for a *Daubert* hearing because he claims that the Government utilized “the latest fad in DNA testing, ‘low copy number’ (LCN) DNA typing, an STR methodology that has not yet been validated as reliable and that the FBI claims is not in fact generally accepted as reliable by the forensic community.” (Def. Mot. at 17). However, the Government denied that the LCN technique was actually used on the evidentiary samples in this case, and submitted the affidavit of Meredith Kitey, Technical Leader for the U.S. Army Criminal Investigation Laboratory in Fort Gilem, Georgia,¹¹ to explain the techniques

⁹Inbreeding refers to the mating of two persons who are more closely related than if they were chosen at random. *See* NRC II, at 98.

¹⁰Substructuring refers to the tendency toward decreasing genetic heterogeneity and allelic independence exhibited by ethnically homogeneous, non-randomly mating populations. In other words “a substructured population may be defined as one in which the probability of a random match between two of its members is greater than the likelihood of such a match between two members of the population at large.” *See United States v. Chischilly*, 30 F.3d 1144, 1153 (9th Cir.1994).

¹¹ Ms. Kitey was previously the DNA Laboratory Manager, Technical Leader and CODIS Administrator for the Prince George’s County Police Department.

that were used, and why those techniques have routinely been found reliable. (Kitey Aff. I). In response, the defense submitted the affidavit of Dr. Dan Krane, a Professor in the Department of Biological Sciences at Wright State University in Dayton, Ohio. (Supp. Reply To Government's Resp. To Mot. To Exclude DNA Test Results And Request For *Daubert* Hr'g, Ex. 1)(hereinafter, "Krane Aff."). Dr. Krane disagreed with Ms. Kitey's definition of LCN testing, and insisted that, at least by his definition, LCN testing *was* performed in this case, and that LCN testing is not currently a reliable procedure under *Daubert*. (Krane Aff. ¶¶ 15-16). The Government then submitted a second affidavit from Ms. Kitey, supplementing her original affidavit, which directly refuted points made by Dr. Krane. (Kitey Aff. II).

Before undertaking an arduous *Daubert* analysis of this relatively new DNA typing technology, the Court first needed to resolve the underlying factual dispute between the parties as to whether LCN testing was employed at all. To that end, the Court held an evidentiary hearing on October 10, 2008, on the limited factual issue of whether LCN testing was performed on the evidentiary samples in this case. It was not a full *Daubert* hearing on the reliability of the LCN procedure. Both Ms. Kitey and Dr. Krane testified by telephone. The Court sought to resolve two disputes that it viewed as essentially factual: (1) What is the proper, scientifically accepted definition of low copy number testing?; and (2) How much DNA was actually present in the evidentiary samples tested by the Prince George's County forensic laboratory in this case?

Upon consideration of all the evidence and affidavits, the testimony of both experts, and the arguments of counsel, the Court concludes that LCN testing was *not* performed in this case, and therefore there is no need for a *Daubert* analysis of that procedure. Because the PCR/STR technique that *was* used is generally accepted as reliable, the evidence is admissible.

1. Dueling Definitions of LCN Testing

According to Dr. Krane, LCN testing refers to DNA tests done on amounts of DNA that are at or below the “stochastic threshold.” (Transcript of Hearing, October 10, 2008, at 12)(hereinafter, “Hr’g Tr.”). This is the “minimum amount of DNA that’s necessary so as to avoid having random processes dominate or manifest themselves in DNA testing results.” (Hr’g Tr. 12). The scientific community has not settled on a precise quantity as the stochastic threshold, but he suggested that “everybody would agree” it is less than half a nanogram, with many suggesting that it is “in the ballpark” of 0.125 nanograms. (Hr’g Tr. 12). Four problematic effects are often seen with testing performed below the stochastic threshold: exaggerated stutter, peak height imbalance, allelic drop-in and allelic drop-out. Dr. Krane argues that these effects must reduce the weight given to the test results in LCN cases.

The defense contends that the Government will be seeking to introduce DNA evidence based on samples quantitated to contain less than 100 picograms¹² of DNA. (Def. Mot. 45). Dr. Krane believes that the “starting template for all of the questioned samples was less than 100 picograms. By definition, therefore, and perhaps unintentionally . . . Prince George’s County DNA Laboratory *did* perform low copy number DNA testing in this case.” (Krane Aff. ¶ 16) (emphasis in original). He continues, “Quite simply, if the starting quantity of DNA prior to the time the PCR amplification (sic) is very small, the PCR process can produce results that are inaccurate and unreliable, especially, as in this case, when mixtures are present.” (Krane Aff. ¶

¹² There are 1,000 picograms in one nanogram. Therefore, 100 picograms is the equivalent of 0.1 nanograms.

16). Although the defense contends that three federal cases have upheld the validity of the Profiler Plus test kit used in this case,¹³ none has addressed the use of the kits when low copy number (less than 100 picograms) of DNA is tested. It takes the position that “the low copy technique used in this case . . . is the methodology at issue, not STR typing in general, and certainly not PCR ‘testing’ in general.” (Def. Mot. 51). Further, it claims that no cases have addressed the admissibility of LCN testing in general, so this is an issue of first impression for the Court, and one for which a *Daubert* hearing should be granted. (Def. Mot. 51).

The Government flatly denies that LCN testing was done in this case. Its position is that LCN testing is not defined only by the fact that less than 100 picograms of DNA are used, but that it also involves a modified process requiring dedicated laboratory space, and this is not what occurred in this case.¹⁴ (Kitey Aff. I ¶ 12).

In his affidavit, Dr. Krane “strongly disagree[d]” with Ms. Kitey’s contention regarding LCN:

The assertion that low copy number (LCN) is a process rather than something that is determined by the quantity of template DNA is incorrect. The one feature that all LCN processes have in common is the knowledge or expectation that less than the recommended amount of template DNA is being used. Using small amounts of template DNA (even without making any changes to the testing process itself) is all it takes for something to be in the LCN category. This principle is well-understood in the scientific community.

(Krane Aff. ¶ 15).

¹³ See *United States v. Gipson*, 383 F.3d 689 (8th Cir. 2004); *United States v. Morrow*, 374 F. Supp. 2d 51 (D.D.C. 2005); *United States v. Trala*, 162 F. Supp. 2d 336 (D. Del. 2001).

¹⁴ At the October 10 hearing, Dr. Krane testified that the modified procedures used when deliberately performing LCN testing include increased polymer rays, additional rounds of amplification, skipping quantitation, and the use of consensus profiles. (Hr’g Tr. 33).

Without making a finding with regard to the dueling definitions of LCN testing advocated by the parties, the Court notes that both experts agree that, *at a minimum*, LCN testing involves testing minuscule amounts of DNA that fall below the (somewhat amorphous) stochastic threshold – around 100 picograms or less. Therefore, ascertaining the amount of DNA present in the evidentiary samples tested in this case has become an issue of critical importance.

2. Relationship of Quantiblot Results to Amount of Template DNA

Both experts agreed that quantitation is an important step in the analysis of DNA evidence because the standardized kits that generate the DNA profiles come with manufacturer's recommendations as to the optimum amount of starting material. Using samples with either more or less than the optimum amount will produce unreliable results. Krane opined that the optimum amount is between 1 and 2 nanograms. (Hr'g Tr. 10). Ms. Kitey testified that at the time the samples in this case were tested, an internal validation procedure conducted at the Prince George's County lab had concluded that the optimal amount of DNA for amplification using these kits was 0.8 nanograms, which is slightly less than the manufacturer's recommendation of 1.0 nanograms. (Hr'g Tr. 46). Dr. Krane conceded, however, that he would expect results at 0.8 nanograms to be roughly consistent with those achieved using 1.0 nanogram. (Hr'g Tr. 29). He also conceded that the Profiler Plus and CoFiler test kits used in this case are widely used by forensic crime labs, and he recognizes them as being scientifically accepted, at least when used with amounts of template DNA that are not low copy. (Hr'g Tr. 28).

Samples N6, N1b, N2d, BG1, and K3 were quantitated using a commercial slot blot kit

called the “Quantiblot” which requires the analyst to estimate the amount of DNA in each sample by comparison with a known reference standard.¹⁵ Both parties agree that this is a visual, inexact comparison that is “not as sensitive as would be preferred.” (Krane Aff. ¶ 10). The defense bases its LCN argument on the fact that for these five samples no visible blot was produced on the Quantiblot gel, so it contends that “the analyst simply took a guess by noting ‘< 0.1 ng.’”¹⁶ (Def. Mot. 16). It argues that the Court is thus left to speculate whether the amount of DNA in each sample was 95 picograms, 10 picograms, or 0 picograms. (Def. Mot. 17).

For sample K1C, which was tested in February 2007, a newer quantitation method known as the “Quantifiler” was used. This test indicated that sample K1C contained 0.1 nanograms of DNA. Dr. Krane then concludes that “[t]he laboratory appears to have departed from the manufacturer’s recommendation of having a minimum of 1 ng of template DNA for PCR amplification and this requires internal developmental validation before the product of the modified procedure can be accepted as reliable.” (Krane Aff. ¶ 10).

The Government’s Supplemental Affidavit from Ms. Kitey argues that Dr. Krane’s argument is wrong because it is “based on a faulty premise: that the concentration of DNA observed on a Quantiblot is equivalent to the quantity of input DNA used during the amplification process.” (Kitey Aff. II ¶ 3). Ms. Kitey believes that Dr. Krane is “incorrectly referring to a number associated with the Quantiblot kit, as opposed to the actual sample amount used in the PCR/STR testing.” (Kitey Aff. II ¶ 4).

¹⁵ The Quantiblot was accepted in the relevant scientific community in 2004 when these tests were performed.

¹⁶ The symbol “<” is read as “less than”.

Ms. Kitey explained that quantitation of DNA using the Quantiblot kit is accomplished by testing a *only a small portion* of the DNA sample and visually comparing the results to standards containing known amounts of DNA (0, 0.156, 0.312, 0.625, 1.25, 5.0, and 10.0 nanograms). Once the forensic examiner estimates the concentration of DNA on the slot blot, the forensic examiner then extrapolates how concentrated the DNA is in the entire sample and dilutes or concentrates the sample accordingly in preparation for PCR/STR testing.”¹⁷ (Kitey Aff. II ¶ 6). At the hearing and in her two affidavits, Ms. Kitey clarified that the Quantiblot result is *not* the same as the amount of DNA tested via PCR/STR. The Quantiblot only quantifies the amount of DNA in the *one microliter sample* that is loaded onto the device. So the results of the slot blot are properly expressed not simply in nanograms, but in *nanograms per microliter*.

For samples N6, N1b, N2d, BG1, and K3, no DNA was detected on the Quantiblot, indicating that the amount was less than 0.156 nanograms, which is the lowest reference point in the kit. The lab notes indicate that the amount of DNA in each of the above samples was less than 0.1 nanograms. Ms. Kitey testified that because the Quantiblot is not as sensitive as analysts would ideally prefer, getting results indicating the presence of less than a tenth of a nanogram of DNA in the one-microliter sample was not unusual, and in her experience, there was often still “plenty of DNA to be tested [in the evidentiary sample].” (Hr’g Tr. 50). The standard practice in Prince George’s County at the time was, if a sample was under the lowest standard on a Quantiblot, analysts would simply load the maximum volume of DNA sample into

¹⁷ Ms. Kitey analogizes the process to estimating the number of apples in a pie by counting the apples in a single slice, then multiplying that by the total number of slices.

the amplification procedure (ten microliters) and obtain results. (Hr'g Tr. 50-51). This standard is reflected in the lab's Standard Operating Procedures. (Hr'g Tr. 59). Ms. Kitey testified that circumstances like this are "more common than not, given . . . what people are trying to obtain DNA from these days." (Hr'g Tr. 59).

In this case, the total targeted amount of DNA to be used in amplification was 0.8 nanograms (800 picograms), "based on the laboratory's internal validation studies as required by the manufacturer and the FBI National Quality Assurance Standards." (Kitey Aff. II ¶ 7). Thus, if the slot blot results for a particular sample were 0.1 nanograms or less per microliter, then the laboratory would have amplified 10 microliters of the remaining evidentiary sample in an attempt to attain the target range of 0.8 to 1.0 nanograms that is actually used in the PCR/STR amplification procedure. (Kitey Aff. II ¶ 7). Therefore, in this case, the actual amount of DNA in each sample tested was *ten times* the amount indicated on the Quantiblot. The only question remaining, then, was to examine the results of the DNA testing to determine whether or not the amount of template DNA appeared to have been at or beneath the stochastic threshold.

3. Analysis of DNA Testing Results

Regardless of her disagreement with Dr. Krane as to the definition of LCN testing, Ms. Kitey's opinion that LCN testing was not performed in this case is based on more than the fact that no modified testing procedures were used. In addition, she does not believe that less than 100 picograms of DNA were tested. Although the Quantiblot indicated that less than 156 picograms were present in each one-microliter sample, the actual amount of DNA tested was ten times that amount. It is far more likely than not, then, that the amount of DNA in the sample was

significantly above the stochastic threshold. (Hr’g Tr. 67). She opined that, “based on the DNA profiles that were obtained of the end product it’s obvious that there was much more than 100 picograms that was input into the system.” (Hr’g Tr. 69).

Dr. Krane criticized Ms. Kitey’s assumption that the “less than 0.1” result is effectively equal to 0.1 nanograms, so that when all 10 microliters were used in the PCR/STR analysis, the total amount would approximate 1.0 nanograms. (Hr’g Tr. 21-22). Dr. Krane urged the Court also to “seriously consider that less than 0.1 nanograms may actually be, oh, I don’t know, .01 nanograms or less, in which case we are certainly entering into things that are at or beneath the stochastic threshold.” (Hr’g Tr. 21-22). Although Dr. Krane seemed to accept Ms. Kitey’s explanation that the actual amount of DNA tested was approximately ten times that reflected on the Quantiblot, he maintains that when the Quantiblot indicates that less than 0.1 nanograms are present, “we can’t say if we are at or beneath that stochastic threshold based on the quantification.” (Hr’g Tr. 31).

Dr. Krane believes that the test results in this case are consistent with those he would expect from tests run with low copy number DNA. For example, he points to “significant amount of locus drop-out,” “some allelic dropout”, and that, in his assessment, the heights of the peaks being tested are “consistently very low.” (Hr’g Tr. 22-23). However, Dr. Krane was unable to say definitively whether LCN testing was performed in this case. In response to the Court’s direct question, Dr. Krane responded: “I see nothing that suggests that it is not, and yet I see many things that suggest that it is.” (Hr’g Tr. 25).

Ms. Kitey argued strongly that the opposite was true – that the results obtained in these tests prove that sufficient template DNA was present in the samples. For example, sample N6

returned a full profile at all 13 loci tested, indicating to her that it was likely that between 0.5 and 1.0 nanograms had been present in the sample. Even for other samples in which only partial profiles were obtained, this result alone does not indicate that less than 100 picograms were used. She stated that “[p]artial profiles occur daily in a forensic laboratory.” (Hr’g Tr. 69). This can be due to insufficient quantity, but also due to other routine occurrences, such as degraded, poor quality template DNA. (Hr’g Tr. 70). In Ms. Kitey’s opinion, the results for the N6, N1b, N2d, BG1 and K3 samples all indicated sufficient quantity. Only one sample had complete allelic drop-out, and that was only at one location. (Hr’g Tr. 72). Even at loci with low peaks, the fact that the tests showed results at most loci indicates that there was enough DNA for the PCR process to work in the first place. Furthermore, Ms. Kitey testified that in her rather extensive experience with forensic DNA testing, she has never seen a full profile obtained from only 100 picograms of DNA without the use of modified procedures. (Hr’g Tr. 71).

4. Conclusion

On the ultimate issue of whether less than 100 picograms of DNA were tested, making this a “low copy number” case, the Court credits the testimony of Ms. Kitey more than that of Dr. Krane. Initially, it appears that the defense and Dr. Krane misinterpreted the relationship between the Quantiblot result and the subsequent PCR/STR amplification, and, on the basis of the Quantiblot result alone, erroneously concluded that the DNA testing had been done with a template amount below the stochastic threshold, transforming this into an LCN case. In reality, the amount of DNA tested was *ten times* the amount shown on the Quantiblot, because 10 microliters of the DNA solution were used, as opposed to the 1 microliter used in the Quantiblot

test. At the hearing, Dr. Krane seemed to concede that the amount of template DNA was ten times that indicated on the Quantiblot, but proceeded to argue that sufficient uncertainty remained about the precise quantity tested that this Court should find that LCN testing had been done, and conduct a *Daubert* hearing to determine the reliability of the test results.

The Court declines to so find. The preponderance of the evidence shows that, while the exact quantity of template DNA present in the samples cannot be known with certainty, there is no basis for the Court to conclude that the starting material contained 0.1 nanograms (100 picograms) or less. To the contrary, the Court finds Ms. Kitey's interpretation of the results convincing, and concludes that a sufficient amount of template DNA was used. In short, this is *not* an LCN case, and therefore no "latest fad" was employed, as alleged by the defense.

The Court further concludes that the PCR/STR analysis conducted in this case has been previously found reliable by other federal courts, and the highest court of Maryland, and that no *Daubert* hearing is needed on that procedure.¹⁸ Therefore, the Defendant's motion to exclude the DNA evidence on the basis of the LCN procedure is denied.

II. STATISTICAL SIGNIFICANCE OF THE COLD HIT MATCH

Defendant next moves to exclude the Government's DNA evidence based on the alleged lack of a reliable statistical interpretation of DNA evidence identified through a "cold hit" from a DNA database. This argument has two parts: First, that DNA evidence should not be admitted in the absence of statistical evidence reflecting the probability of a coincidental match. Second,

¹⁸ See, e.g., *United States v. Wright*, 215 F.3d 1020, 1027 (9th Cir. 2000); *United States v. Beasley*, 102 F.3d 1440, 1447-48 n.4 (8th Cir. 1996); *United States v. Morrow*, 374 F. Supp. 2d 51 (D.D.C. 2005); *United States v. Ewell*, 252 F. Supp. 2d 104, 111-12 (D.N.J. 2003); *Young v. State*, 879 A.2d 44 (Md. 2005).

because there is no agreement on a single method for calculating the likelihood that a cold hit is actually a coincidental match, there are no admissible statistics to accompany the Government's evidence in his case. Therefore, the Defendant argues that the Court should exclude all the DNA evidence against him. For the reasons below, the Defendant's arguments are unconvincing.

A. Necessity of Statistics to Contextualize DNA Evidence

The Defendant argues that DNA evidence must be presented with accompanying statistics to help a jury properly determine the weight and relevancy of that evidence. Primarily, this involves answering “the coincidence question,” – i.e., what is the chance that this defendant's DNA profile might coincidentally, but incorrectly, match the evidentiary profile? As the Supreme Court of California has stressed:

A determination that the DNA profile of an evidentiary sample matches the profile of a suspect establishes that the two profiles are consistent, but the determination would be of little significance if the evidentiary profile also matched that of many or most other human beings. The evidentiary weight of the match with the suspect is therefore inversely dependent upon the statistical probability of a similar match with the profile of a person drawn at random from the relevant population.

People v. Venegas, 954 P.2d 525, 548-49 (Cal. 1998); *see also United States v. Jenkins*, 887

A.2d 1013, 1016 (D.C. 2005) (“evidence of a DNA match is made more probative when it is introduced in conjunction with statistical evidence that expresses the significance of the match”).

The Government has not contested this premise of Defendant's argument.

The Court agrees that DNA evidence cannot be admitted in a vacuum; the Government must also present some additional information with which a jury can accurately assess the significance of the consistency between a defendant's DNA profile and that of the evidence. The precise nature of the requisite information will be discussed *infra*.

B. Unique Aspects of Cold Hit DNA Evidence

Providing jurors with proper context when the DNA profile match flows from a “cold hit” in a database presents unique challenges. Many laypersons may try to analogize a cold hit DNA match to a match between a fingerprint recovered from a crime scene and one on file in a similar type of database. Fingerprint identification evidence is familiar to most people, and since the value of a fingerprint identification is not reduced by virtue of the utilization of a large database, most would conclude that DNA profile matches should also be accepted. While understandable, this assumption is incorrect. Unlike DNA profiles, fingerprints are assumed to be completely unique, even when compared to close relatives. Thus, a match between an evidentiary print and a database print can only mean that the prints came from the same individual; no other conclusions are possible. However, DNA profiles are composed of only a few loci out of the millions that constitute an individual’s entire genetic make-up. Because these partial profiles are *not* assumed to be unique, especially among close relatives, the possibility of coincidental matches and their probabilities must be taken into account, and the significance of a cold hit DNA match differs from a cold hit fingerprint match, and from a DNA profile match between an evidentiary sample and a single suspect.

Dr. Dan Krane, the defense expert, provided the following succinct explanation of the difference between what he described as “probable cause” hits and “cold hits”:

A “match” between the DNA profiles of two different samples means little without accompanying data on both the chance of coincidental matches and the possibility of false positives. Until recently, the DNA profiles that have been generated for forensic purposes have been almost exclusively those that could be characterized as “probable cause matches,” in which DNA testing has been performed upon a reference sample taken from a suspect that has already been

linked to a crime by direct or circumstantial evidence. A new category of DNA profile “matches” are becoming increasingly common however – those that are generated as a result of “cold hits” that result from the trawling of a large number of DNA profiles maintained in databases (usually those of previously convicted offenders). Since the primary difference between these kinds of matches is the manner in which a suspect is first identified, it is generally accepted that it is not possible to convert one type of case into the other (for instance, by simply retesting a reference sample once a “cold hit” has been identified). It is also generally accepted in the scientific community that the statistical significance of those two kinds of DNA profiles matches should be determined differently.

(Krane Aff. ¶ 18).

In most probable cause cases, the only statistical calculation presented along with DNA match evidence is one utilizing the “product rule.”¹⁹ After profiling a specific number of loci on a strand of DNA, the analyst obtains, from published tables, the frequencies of variations in genetic material at each tested locus. The frequencies of all the tested loci are then multiplied together to obtain the frequency with which that particular profile is seen in various population groups. In probable cause cases, this number expresses two distinct concepts, though they happen to coincide: 1) the expected frequency, or rarity, of that particular DNA profile in the population; and 2) the chance that the suspect’s DNA profile might coincidentally, but incorrectly, match the evidentiary profile (the “random match probability” or “RMP”). In probable cause cases, the product rule therefore indicates the rarity of the particular profile *and* answers the “coincidence question.”

In cold hit cases, it is generally accepted that the rarity of the evidentiary profile does not change, and is still calculated via the product rule. However, because the search of the database increases the odds that a coincidental match will be found, the product rule calculation does *not*

¹⁹The product rule provides that if two events are independent of each other, the probability of each occurring can be multiplied, and the resulting product is the probability of both events occurring. *See United States v. Jenkins*, 887 A.2d 1013, 1018 n.6 (D.C. 2005).

express the likelihood that a cold hit match is coincidental. What is not settled is the best way to calculate a similar “random match probability” for cold hit cases. An overwhelming number of scientific authorities agree that searching a large database of DNA profiles requires a novel statistical methodology to derive the significance of that type of match. *See, e.g.*, NRC II at 134 (“There is an important difference between [a “probable cause” case] and one in which the suspect is initially identified by searching a database to find a DNA profile matching that left at a crime scene. In the latter case, the calculation of a match probability . . . should take into account the search process.”).

Defendant argues that because the product rule RMP is not generally accepted as a reliable way of expressing the likelihood that a cold hit match is coincidental, the Court should conduct a *Daubert* analysis of the various proposed methodologies for expressing that concept.

C. Statistical Calculations Concerning Cold Hit Matches

There are at least three calculations that could potentially be presented along with evidence of a cold hit match to provide the appropriate context for the jury.

The first approach was proposed by the National Research Council in 1992 (“NRC I”).²⁰ This method corrects for ascertainment bias (the bias that exists when one searches for something rare in a set database) by using one set of loci to screen for and identify a suspect in a database, then using a different set of loci to confirm a match. Statistical analysis using the product rule would then be done on only the *second* set of loci. This result is generally agreed upon as reliable, though conservative, because it uses fewer loci in the calculation of the

²⁰ National Research Council, DNA Technology in Forensic Science (1992). The National Research Council is an arm of the National Academy of Sciences.

statistical significance of the match, resulting in “shorter odds” than if all loci were considered.²¹ This approach is considered valid, though not optimal, because there may be other valid methods that use more or all of the testable loci in determining the statistical significance of a match. *See Nelson*, 185 P.3d at 62.

The National Research Council proposed another method just four years later. (“NRC-II”).²² This approach calculates the odds of finding a match in a given database by multiplying the expected frequency of the profile (the rarity statistic, derived using the product rule) by the number of profiles in the database. This statistic has been called the “database match probability.” This result would be the expected frequency of the profile in a sample the size of the database and thus the chance of randomly finding a match in a sample of that size. The database match probability has the most impact on the reliability of a cold hit match when few loci are tested because one is obviously more likely to find a coincidental match at seven or eight loci than at twelve or thirteen, and this likelihood only increases with the number of profiles

²¹ Not surprisingly, the Defendant urges the Court, if it finds the DNA evidence otherwise admissible, to adopt the NRC I approach, i.e., to rule that some locations on the DNA strand may be used to make the “cold hit” and different locations on the DNA strand should be used to determine the correctness of the “hit” and to generate a random match probability estimate. This would be advantageous to the Defendant because if all the loci used in the cold hit match are then excluded from the calculation used to give the jury an estimate of the likelihood of coincidence, this will cause the coincidence probability to be greater. For example, if 8 of the 13 CODIS loci were used in the comparison producing the cold hit, then there would be only 5 left to calculate the probability of the crime scene evidence being left by another random person. The probability that a random stranger will match the defendant at 5 loci will clearly be higher than the probability that a stranger would match the defendant at 13 loci.

As discussed below, the Court does not find it appropriate to find one method admissible to the exclusion of the others. In any case, the Defendant has provided no evidence or argument as to why the NRC I approach should be considered superior. In fact, the *Jenkins* court did not extensively address this approach, saying it was “no longer accepted or followed by the relevant scientific community.” 887 A.2d at 1022 n.17.

²² National Research Council, The Evaluation of Forensic DNA Evidence (1996)

compared.²³ *See People v. Nelson*, 185 P.3d 49, 62-63 (Cal. 2008). Arguably, this approach requires presentation to the fact-finder of *both* the rarity statistic *and* the database match probability.²⁴

The third method is known as either the Balding-Donnelly method (after the names of its two leading advocates), or the Bayesian method (named for the 19th-century inventor of the formula used). Instead of focusing on the probability of finding a match in a given database, this formula focuses on the elimination of other profiles during the search. Thus, the match becomes *more* significant with greater database sizes because the elimination of other known persons increases the chances that the identified suspect is actually the source of the sample DNA. Thus, a database match has a slightly *higher* probability of identifying the source of the evidentiary DNA than would be expected from the standard product rule calculation.

D. Differences Between Statistical Methods Impact Relevancy, Not Admissibility

Each of the above methods for expressing the significance of a cold hit match has its advocates and detractors. Defendant argues that the absence of consensus as to the most “reliable” statistical methodology should preclude the Government from offering *any* DNA evidence in the case, or, at the very least, preclude use of “inappropriate likelihood ratios currently attached to sample BG1 (Jeep steering wheel cover). ” (Def. Mot. at 78-80). This issue

²³ For example, suppose the rarity of a profile in a crime scene sample was calculated as 1 in 1 million. If a single suspect were compared, a match would be extremely unlikely unless the suspect were, in fact, the source of the sample. However, if the sample was instead compared with a database containing 100,000 profiles, the chances of finding a match reduce to 1 in 10, even if the true offender is not in the database.

²⁴ This is the interpretation suggested by the FBI DNA Advisory Board. *See Nelson*, 185 P.3d at 63 (citing *Jenkins*, 887 A.2d at 1020).

has not been addressed by a federal court, but has been resolved by the high courts of both California and the District of Columbia. *See People v. Nelson*, 185 P.3d 49 (Cal. 2008); *United States v. Jenkins*, 887 A.2d 1013 (D.C. 2005).

Jenkins and *Nelson* did not apply the *Daubert* standard to the question of the statistical interpretation of cold hit matches. *Jenkins*, 887 A.2d 1013 (applying *Frye* test); *Nelson*, 185 P.3d 49 (applying *Kelly* test).²⁵ However, their holdings are still very instructive. Those courts concluded that the issue being raised by the defendant (identical to the issue being raised here) pertained to the *relevance* of the competing calculations, not to the *soundness* of the methodology:

At the heart of this debate is a disagreement over the competing questions to be asked, not the methodologies used to answer those questions. The rarity statistic, the database match probability, and the Balding-Donnelly approach each answer unique and potentially relevant questions. More importantly, there is no controversy in the relevant scientific community as to the accuracy of the various formulas. In other words, the math that underlies the calculations is not being questioned. Each approach to expressing significance of a cold hit DNA match accurately answers the question it seeks to address. The rarity statistic accurately expresses how rare a genetic profile is in a given society. Database match probability accurately expresses the probability of obtaining a cold hit from a search of a particular database. Balding-Donnelly accurately expresses the probability that the person identified through the cold hit is the actual source of the DNA in light of the fact that a known quantity of potential suspects was eliminated through the database search. These competing schools of thought do not question or challenge the validity of the computations and mathematics relied upon by the others. Instead, the arguments raised by each of the proponents simply state that their formulation is more probative, not more correct. Thus, the debate cited by Mr. Jenkins is one of relevancy, not methodology[.]

Jenkins, 887 A.2d at 1022-23. The court then found that under its *Frye* test, there was no basis to exclude the DNA evidence.

²⁵ The Court notes that Dr. Krane testified in both of these cases, and Dr. Mueller, who also submitted an affidavit on behalf of the Defendant in this case, also testified in *Nelson*.

Nelson followed *Jenkins*, also finding that cold hit statistics were an issue of relevancy, and that the RMP derived from the product rule was still relevant and admissible as an expression of *the rarity of the evidentiary profile*. However, the *Nelson* court further clarified that:

The conclusion that statistics derived from the product rule are admissible in a cold hit case does not mean that they are the only statistics that are relevant and admissible. The database match probability statistic might also be admissible. As explained, it is unlikely the database match probability statistic would have been significant to the jury in this case given the size of even that number. But in a different case, if the database were large enough and the odds shorter than those here, the database match probability statistic might also be probative. Nothing we say prohibits its admission.

Nelson, 185 P.3d at 66 n.3 (emphasis added) (internal citation omitted).

This Court agrees with the *Jenkins* and *Nelson* decisions and concludes that there is no basis under *Daubert* or the Federal Rules of Evidence to exclude evidence of the DNA matches in this case. However, the Government shall only be permitted to present the product rule calculation as an expression of the rarity of the profile, but not as an expression of the random match probability, i.e., the answer to the “coincidence question.” If the defense wishes to present statistical experts utilizing one or more of the above methods to argue that the match is deserving of less weight because it was obtained through a database search, it is free to do so. Ultimately, it shall be for the jury to decide the appropriate weight to assign to the forensic evidence.

IV. MISCELLANEOUS ARGUMENTS

A. Procedural Precautions and the Possibility of Error During the Testing Process

The defense contends that the Court should hold a hearing under Rule 702 and *Daubert* to determine whether the Government’s evidence is reliable and whether all steps of the DNA

typing methodology used in this case were correctly performed. (Def. Mot. 52). The defense argues that PCR/STR DNA testing is a complicated and highly technical procedure that requires a series of distinct steps, and that each step is typically governed by multi-faceted protocols. It says that *each step* is subject to independent review, and the third prong of Rule 702 requires that the Court be convinced that “the witness has applied the principles and methods reliably to the facts of the case.” (Def. Mot. 52); Fed. R. Evid. 702.

The Government contends that these arguments essentially challenge the proficiency of the tester rather than the reliability of the test, so they go to the weight of the Government’s evidence, not its reliability/admissibility. (Resp. 65). *See United States v. Beasley*, 102 F.3d 1440, 1448 (8th Cir. 1996); *Ewell*, 252 F. Supp. 2d 104, 114 (D.N.J. 2003); *United States v. Shea*, 957 F. Supp. 331 (D.N.H. 1997). The Court agrees, and therefore concludes that the defense’s speculative assertions on this point do not require the exclusion of the evidence or a *Daubert* hearing under Rule 702.

Furthermore, laboratory error may form the basis of exclusion only when a reliable methodology was so altered by the laboratory as to skew the methodology itself. *See Beasley*, 102 F.3d at 1448; *Ewell*, 252 F. Supp. 2d at 113. In its motion, the Defendant makes few concrete allegations as to error or failure to follow protocol, but wants the Court to hold an evidentiary hearing to ascertain *if* certain procedures were followed. (Def. Mot 120, 123, 131, 140, 142). As the *Daubert* court stated, “vigorous cross examination, presentation of contrary evidence, and careful instruction on the burdens of proof are the traditional and appropriate means of attacking shaky, but admissible evidence.” *Daubert*, 509 U.S. at 596. Therefore, on this point, the defense motion is denied.

B. Interpretation of Testing Results for Samples N1b, N2d, and K1C

No statistical estimates were calculated for three of the evidentiary samples: N1b (trigger and grips of Glock), N2d (trigger and grips of Glock); and K1C (Pontiac Grand Am shifter). However, the analysts concluded that Mr. Davis' DNA profile was "consistent" with "several" parts of the evidentiary profiles, and/or that Mr. Davis "cannot be excluded" as the source of the evidentiary samples. The Defendant challenges the admissibility of any opinions regarding samples N1b, N2d and K1C without any supporting statistics whatsoever. The Court sees this argument as having two parts: (1) Whether DNA evidence of this type may be admitted without an accompanying statistical analysis; and (2) Whether the specific opinions contained in the lab reports are admissible.

First, the defense argues that in the vast majority of federal cases in which DNA evidence of this type has been admitted, the evidence of a DNA match is accompanied by statistical information. *See, e.g., United States v. Wright*, 215 F.3d 1020, 1025 (9th Cir. 2000); *United States v. Ewell*, 252 F. Supp. 2d 104, 113 n.2 (D.N.J. 2003); *United States v. Gaines*, 979 F. Supp. 1429, 1431-32 (S.D. Fla. 1997). A number of state appellate courts have considered whether DNA evidence is admissible in the absence of statistical data; with very few expectations, those courts have also required that statistics be presented as a condition of admissibility. *See, e.g., Nelson v. State*, 628 A.2d 69, 76 (Del. 1993); *State v. Williams*, 574 N.W.2d 293, 298 (Iowa 1998). *But see Young v. State*, 879 A.2d 44 (Md. 2005)(admitting expert report concluding that defendant was "source" of DNA without any accompanying statistics). In addition, a number of legal commentators have suggested that the admissibility of DNA evidence depends on having scientifically valid statistics on the frequency of the matching profiles. *See, e.g., David L. Faigman, et al., 4 Modern Scientific Evidence: The Law and*

Science of Expert Testimony 30:14 (2005-2006 ed.) (“Unless some reasonable explanation accompanies testimony that two profiles match, it is surely arguable that the jury will have insufficient guidance to give the scientific evidence the weight it deserves.”); Kenneth S. Broun, et al., 1 McCormick on Evidence § 210 (6th ed. 2006) (“Without being informed of such background statistics, the jury is left to its own speculations.”).

The Court agrees with the numerous courts and authorities that have concluded that DNA evidence purporting to inculcate a defendant must be accompanied by some sort of explanation as to the significance of the consistency. Without such context, “the jury does not know what to make of the fact that the patterns match: the jury does not know whether the patterns are as common as pictures with two eyes, or as unique as the Mona Lisa.” *United States v. Ye*, 134 F.R.D. 161, 181 (N.D. Ohio 1991). Therefore, the Court holds that evidence concerning these three samples will not be admitted unless the Government can provide reliable accompanying statistics explaining approximately how many persons in the general population would be “consistent” with this partial profile, and/or how many persons in the general population “cannot be excluded” based on the partial profile.

Second, with respect to the use of the contested terminology used in the analyst’s report regarding samples N1b, N2d, and K1C, Ms. Kitey explained:

DNA typing is an exclusionary test. We try to exclude individuals from profiles. When we cannot exclude, we must then comment on what we do see in the profile. The profiles obtained from these items of evidence are actually mixtures of partial profiles. There is enough information present in the profiles to exclude most of the individuals associated with the case. The statement above is a true and accurate statement. We were not able to exclude Davis and/or Moore from these samples, but because of the limited nature of the profiles, no statistical calculations were performed, and no further conclusions were made.

(Kitey Aff. I ¶ 14(a)).

She then quotes Dr. John Butler, an expert quoted extensively in the Defendant's motion:

Of course obtaining matching alleles between a full-profile suspect and a partial profile evidentiary sample is not as powerful as a full-profile to full-profile match. However, any data is better than none. Even if the results are obtained on only a few STR loci, this information can provide ample assistance to either include or exclude the suspect and therefore aid in resolving the case.

(Kitey Aff. I ¶ 14(a)) (quoting John Butler, Forensic DNA Typing: Biology, Technology and Genetics of STR Markers 526 (2d ed. 2005)).

The Court concludes—provided that the Government presents an appropriate statistical analysis for these samples—that the expert's opinions that the profiles are “consistent” or that the Defendant “cannot be excluded” are admissible. While this evidence is certainly deserving of less weight than a full-profile to full-profile match, the Court is convinced that the opinions here were the product of a reliable methodology. The Court need not conclude that the expert's opinion is *correct*, only that it is reliable and helpful to the factfinder. Thus, on this second prong of its argument, the defense's objections to the characterization of the DNA test results go to the weight, but not the admissibility of the evidence.

Next, the defense raises an objection to the same evidence because it alleges that application of reliable principles and methods “leads only to the conclusion that Mr. Davis . . . [is] excluded as the source” of the N1b and N2d samples. Ms. Kitey states that exclusion is *not* a proper conclusion to be drawn from these samples. These samples yielded partial profiles, and with limited samples, allelic drop-out is expected. Thus, an individual is not excluded from a partial profile simply because some of the alleles are not detected. (Kitey Aff. I ¶ 14(b)). She noted that the conclusions with respect to these samples were subjected to and agreed upon during peer review. (Kitey Aff. I ¶ 14(b)).

This seems to be a complaint about the *results* reached by the Government's experts and

not their *methods*, so this argument appears to be inappropriate for the Court to resolve at this juncture. A district court need not determine that the proffered expert testimony is irrefutable or certainly correct. *See United States v. Moreland*, 437 F.3d 424, 431 (4th Cir. 2006). Rather, the proper inquiry is whether the particular opinion is based on valid reasoning and reliable methodology. *See TFWS v. Schaeffer*, 325 F.3d 234, 240 (4th Cir. 2003) (“In applying *Daubert*, a court evaluates the methodology or reasoning that the proffered scientific or technical expert uses to reach his conclusion; the court does not evaluate the conclusion itself.”). Therefore, the Court will not exclude the proffered evidence on this basis.

C. Source Attribution Statements

For two of the evidentiary samples, N6 (the ballcap) and K3 (the Pontiac Grand Am steering wheel cover), the analyst interpreting the results has opined that: “To a reasonable degree of scientific certainty, in the absence of an identical twin, Earl Davis is the source of this DNA.” (hereinafter, the “source attribution statements”). The defense requests that the Court preclude the Government from presenting this source attribution statements, and asks that the expert’s testimony be limited to the presentation of a reliable statistical probability figure. (Def. Mot. 106). It argues that such an opinion does not concern reliable “scientific, technical, or other specialized knowledge” within the meaning of Rule 702 and *Daubert*, and will not be helpful to the trier of fact because it is more prejudicial, misleading, and confusing than probative under Rule 403.

The Government’s expert, Ms. Kitey, states that since 2000, the FBI has routinely used source attribution statements to “simplify the ‘match statement’ for a jury when the statistical frequencies calculated for a sample are more than 100 times greater [than] the population of the

United States.” (Kitey Aff. I ¶ 14(e)). This equates to about 1 in 300 billion.²⁶ She says that the use of source attribution statements is “a valid scientifically accepted opinion today.” (Kitey Aff. I ¶ 14(e)).

The defense submitted affidavits from three experts in an effort to refute Ms. Kitey’s position on the use of source attribution statements. Dr. Dan Krane’s affidavit argues that source attribution statements are inappropriate based on 13-locus STR profile matches absent definitive conclusions that (1) no relatives of the individual found to have a matching profile are reasonable alternative contributors of the evidentiary material; and (2) there were absolutely no errors in the testing and interpretation of the evidence samples. Further, Dr. Krane maintains that it is unreasonable to consider the possibility that the contributor of the evidence sample was not from a different population than those for which random match probability statistics have been generated.²⁷ (Krane Aff. ¶¶ 30-36). Dr. Sandy Zabell contends that the source attribution statement has no generally accepted meaning, and simply replaces scientifically-based RMP with a vague qualitative phrase. (Supp. Reply To Government’s Resp. To Mot. To Exclude DNA Test Results And Request For *Daubert* Hr’g, Ex. 2 ¶ 23). Dr. Laurence Mueller objects to source attribution statements primarily on the basis that they do not account for the possibility of laboratory error (i.e., false positives). (Supp. Reply To Government’s Resp. To Mot. To Exclude DNA Test Results And Request For *Daubert* Hr’g, Ex. 3 ¶¶ 13-14).

Under Rule 702, the burden of establishing qualification, reliability, and helpfulness rests

²⁶In this specific case, the allelic frequencies for the evidentiary samples were calculated to be even more rare – in the quadrillions to quintillions. (Kitey Aff. I ¶ 14(e)).

²⁷In this case, probability statistics were generated for three sub-population groups – Caucasians, African-Americans, and Southeast Hispanics.

on the proponent of the expert opinion. *See United States v. Frazier*, 387 F.3d 1244, 1260 (11th Cir. 2004). Expert testimony is admissible under Rule 702 if it (1) concerns scientific, technical, or other specialized knowledge that (2) will aid the trier of fact to understand or resolve a fact in issue. *See Daubert*, 509 U.S. 579; *United States v. Moreland*, 437 F.3d 424, 430-31 (4th Cir. 2006). The first prong of this inquiry necessitates an examination of whether the reasoning or methodology underlying the expert's proffered opinion is reliable—that is, whether it is supported by adequate validation to render it trustworthy. *See Daubert*, 509 U.S. at 590 & n. 9. The second prong of the inquiry requires an analysis of whether the opinion is relevant to the facts at issue. *See id.* at 591-92.

Although it does not contest that the source attribution statements would be relevant under the second prong of the *Daubert* inquiry, the defense urges the Court to find the source attribution statements unreliable for two reasons. First, coincidental matches between profiles of unrelated individuals found within the Arizona state and Prince George's County, Maryland databases—despite astronomical RMP calculations—cast doubt on the certainty with which the statements are made. (Def. Mot. 100-02). In the prior proceedings in this case, a state court judge ordered the Maryland State Police CODIS director to search the Maryland DNA database against itself and determine the number of pairs of profiles that matched at 9 to 13 loci. On January 31, 2007, Maryland CODIS administrator Michelle Graves produced a declaration indicating that the search indicated 21 matches at 9 loci; 3 matches at 10 loci; 1 match at 11 loci; 4 matches at 12 loci; and 3 matches at 13 loci. (Def. Mot. Ex. 16). A number of these matches were explained by the presence of identical twins or close relatives in the database, but several were between completely unrelated individuals. (Def. Mot. Ex. 16). One individual in the Prince George's

County database matched two other unrelated individuals at seven loci, an event that, according to the product rule, produced a RMP of 1 in 1 trillion. (Def. Mot. Ex. 15). Dr. Mueller, upon reviewing this data, opined that the fact that coincidental matches were found in the Prince George's County database, containing less than ten thousand profiles, shows that statements or inferences of uniqueness can be fundamentally incorrect. (Def. Mot. 101-02 & Ex. 14).

Second, the Defendant argues that the FBI's use of source attribution statements is not generally accepted in the scientific community, and is at fact at odds with the practice of numerous other DNA laboratories both within and outside the United States. Highly respected laboratories such as the Connecticut State Crime Laboratory, the Orange County, California police laboratory, the Virginia and Michigan state crime labs, and several international common law jurisdictions reject the use of source attribution statements. (Def. Mot. 102-04) (citing authorities). Additionally, at least one federal district court has noted that, in most cases, "DNA evidence of a 'match' is only admitted with statistical evidence of the probability of a coincidental match, not as a definitive statement." *United States v. Green*, 405 F. Supp. 2d 104, 109 n.4 (D. Mass. 2005).

The defense states that to the best of its knowledge, this type of expert opinion evidence has never been admitted in a federal case over the objection of defense counsel.²⁸ (Def. Mot. 94). However, a nearly identical source attribution statement *was* recently found admissible by the highest court of Maryland in *Young v. State*, 879 A.2d 44 (Md. 2005) ("when a DNA method analyzes genetic markers at sufficient locations to arrive at an infinitesimal random match

²⁸ Notably, the defense cites no cases for this proposition, and the Court has not been able to find any federal cases *excluding* such evidence on the basis of a defense objection.

probability, expert opinion testimony of a match and of the source of the DNA evidence is admissible”). In *Young*, the defendant was charged with a sex offense against a child, and his DNA profile was compared with the evidentiary DNA profile derived from the semen recovered from the victim’s body. At the trial, the State’s forensic DNA analyst testified that the two DNA profiles “matched,” but did not provide any basis for his conclusion. He did not testify to the probability that a random person’s profile would have matched the profile recovered from the victim. 879 A.2d at 45. The expert was not permitted to testify that the defendant was the “source” of the evidentiary DNA. *Id.* at 46. However, the trial court also admitted the expert’s written report, over the defendant’s objection. The report stated that the samples were compared at 13 loci using the Profiler Plus and Cofiler test kits, and that “[t]o a reasonable degree of scientific certainty (in the absence of an identical twin), [the defendant] is the source of the DNA obtained from the sperm fraction of the Anal Swab.”²⁹ *Id.* It contained no statistical data to support this conclusion. *Id.*

The Court of Appeals of Maryland first acknowledged that DNA evidence cannot be *conclusively* attributed to one person unless the entire DNA molecule is analyzed because unrelated individuals can have identical fragments at the targeted loci. However, it held that under “certain circumstances . . . new technologies result in infinitesimal random match probabilities that would be deemed conclusive by all but mathematicians and philosophers.” *Id.* at 52. The court then conducted a careful comparison of the evolving opinion in the scientific community concerning the use of source attribution statements (or, declarations of “uniqueness”), as shown by the difference between the conclusions reached in the NRC I in 1992

²⁹ The Court notes that in the instant case, the test kits used, number of loci tested, and language in the expert’s report are identical to those in *Young*.

and the NRC II in 1996. In 1992, the National Research Council “unambiguously presented accompanying statistical testimony as necessary and emphasized the inappropriateness of testifying to the uniqueness of the genotype.” *Id.* at 53. By 1996, however, the Council acknowledged that because scientific advances now permit the comparison of genetic markers at many more loci than previously possible,

Opinion testimony about uniqueness would simplify the presentation of evidence by dispensing with specific estimates of population frequencies or probabilities. If the basis of an opinion were attacked on statistical grounds, however, or if frequency or probability estimates were admitted, this advantage would be lost. Nevertheless, *because the difference between a vanishingly small probability and an opinion of uniqueness is so slight, courts that decide on a criterion for uniqueness and determine that the criterion has been met may choose to allow the latter along with, or instead of, the former, when the scientific findings support such testimony.*

Id. at 54 (quoting NRC II at 194-95)(emphasis added).

The *Young* court recognized that “there is no bright-line standard in law or science that can pick out exactly how small the probability of the existence of a given profile in more than one member of a population before assertions of uniqueness are justified.” *Id.* (quoting NRC II at 194-95). It concluded, however, that when thirteen STR loci are analyzed, as in the instant case, the random match probability for related individuals, even including siblings, is sufficiently low that the profile may be characterized as unique. *Id.* at 57. Under those circumstances, then, there is no scientific basis for requiring statistical testimony to accompany an expert’s opinion that two profiles “match,” and the expert may contextualize his opinion with nothing more than a statement that to a reasonable degree of scientific certainty, the defendant is the “source” of the evidence. *Id.* at 54, 56. *Accord State v. Buckner*, 941 P.2d 667 (Wash. 1997) (en banc) (“there should be no bar to an expert giving his or her expert opinion that, based upon an exceedingly

small probability of a defendant's DNA profile matching that of another in a random human population, the profile is unique. As in the case of all expert testimony, the opposing side will be able to challenge the expert's opinion and present its own experts.'').

The Court finds the reasoning in *Young* very persuasive, and concludes that in this case—even though there is no bright-line point at which this result is mandated—the random match probability figures calculated for samples N6 and K3 are sufficiently low so that the profile can be considered unique. Ms. Kitey's affidavit states that FBI policy only permits the use of source attribution statements when the random match probability is calculated as at least one hundred times the size of the entire population of the United States, or approximately 1 in 300 billion. (Kitey Aff. I ¶ 14(e)). This Court finds that figure sufficiently infinitesimal that the Government's expert may opine, consistent with *Daubert* and Rule 702, that the Defendant is the source of these samples, and the report containing the challenged phrase is admissible.

This holding is not inconsistent with the Court's above conclusion in Section III.A, *supra*. There, the Court stressed that jurors require assistance contextualizing the significance of the "consistency" between the defendant's DNA profile and the evidentiary profile. This is usually accomplished by presenting a statistical estimate of the profile's regularity or rarity in a given population. The Court now simply builds upon that foundational principle by holding that when the random match probability becomes infinitesimally small, the profile is *so* rare that it may reasonably and rationally be considered unique. In these circumstances, where the random match probability between the two samples is less than 1 in 300 billion, the Court now holds that the appropriate context may be provided to the jury in the form of a source attribution statement.

The Court thus agrees with the holding in *Young* that there is no legal or scientific

requirement that a source attribution statement (or opinion that a profile is “unique”) must be explained or accompanied by the presentation of the random match probability figure or other statistical calculation. However, the Court does have broad discretion under the Federal Rules of Evidence, to ensure that evidence is presented in an effective and efficient manner. *See* Fed. R. Evid. 601(a) (“The court shall exercise reasonable control over the mode and order of interrogating witnesses and presenting evidence so as to (1) make the interrogation and presentation effective for the ascertainment of the truth [and] (2) avoid needless consumption of time.”). In addition, under Rule 705, an “expert may testify in terms of opinion or inference and give reasons therefor without first testifying to the underlying facts or data, *unless the court requires otherwise.*” (emphasis added).

In light of the unique aspects of this case (i.e., the identification of the Defendant by a cold hit in a database and related questions of statistical significance), the Court believes this is a situation in which the Court should “require otherwise.” The Court anticipates and expects that the Defendant will vigorously cross-examine the Government’s expert on the statistical basis for her source attribution statement. Thus, in the interest of time and clarity, the Court will order that the Government, in its direct examination, *also* present the information that forms the basis for the conclusion that the Defendant is the source of the evidentiary DNA sample(s). The Defendant will then remain free to challenge the expert’s conclusion through cross-examination regarding such topics as differing statistical analyses, laboratory error rates, contamination, and any other and concerns he may have. *See Young*, 879 A.2d at 57.

The Court is aware that requiring the Government to provide statistics alongside its source attribution statement somewhat undermines the purpose of presenting such an opinion,

which is to greatly simplify a complex scientific and mathematical concept for lay jurors. However, the Court anticipates that the defense will aggressively challenge the Government's expert on "statistical grounds," and therefore, as the *Young* court stated, that "advantage [will] be lost" already. *Id.* at 54 (quoting NRC II at 194-95). The Government will therefore not suffer any further prejudice if required to provide statistics of its own with which the jury can assess the soundness of the expert's opinion and evaluate the merit of the challenges made on cross-examination. Indeed, in this case, providing the statistical bases for the source attribution statements will strengthen, not weaken, the statements and make them more, not less, understandable for the jury.

The defense next contends that even if the Court finds the source attributions statements admissible under Rule 702, it should still preclude their admission under Rule 403. It argues that because of the "powerful and potentially misleading effect of expert evidence," the source attribution statements should be excluded because their probative value is substantially outweighed by their potential to confuse or mislead the jury.

The Court is mindful that "expert testimony may be assigned talismanic significance in the eyes of lay jurors, and, therefore, the district courts must take care to weigh the value of such evidence against its potential to mislead or confuse." *Frazier*, 387 F.3d at 1263. Some courts and commentators have worried that, particularly in cases where a large amount of statistical and scientific evidence will be presented, if the Government were permitted to present a source attribution statement as facially simple and definitive as "the defendant is the source of the DNA," jurors would "simply 'jump' to the bottom line . . . without giving any meaningful consideration to any dispute over the principles, which underlie the methodology used to

generate” the expert’s conclusion. *United States v. Porter*, 1991 WL 319015 (D.C. Sup. Ct. 1991), *vacated and remanded*, 618 A.2d 629 (D.C. 1992). According to this argument, a source attribution statement would effectively overwhelm a defendant’s attempts to challenge the expert’s findings, insofar as such challenges would have to delve into statistical matters that lack the same certainty and gravity with jurors, and that this problem cannot be overcome through cross-examination alone.

This argument might give the Court more pause if the Government in this case would be presenting naked source attribution statements. However, as the Court has directed that the Government also provide the statistical basis upon which the source attribution statements are made, the concern that jurors would simply latch onto the expert’s conclusion without examining it with a critical eye is greatly mitigated. The Defendant *will* be able to adequately challenge the Government expert’s findings and conclusions through cross examination. Therefore, the probative value of the source attribution statements is not substantially outweighed by the potential to confuse or mislead the jury, and the Court will not exclude the statements under Rule 403.

Therefore, the Court concludes that the source attribution statements are admissible, but will direct the Government to also present the statistical rarity figures calculated for the N6 and K3 samples.

D. Residual Arguments

The defense makes several additional arguments why the DNA evidence should be excluded. First, it argues that all statistical probability calculations should be excluded because the analysis was improperly restricted to only Caucasians, African Americans, and Southeast

Hispanics. (Def. Mot. 61). Next, it argues that the statistics should also be excluded because they fail to include any measure of laboratory error rate. (Def. Mot. 61-62). In addition, the defense argues that the test results are unreliable because the Prince George's County DNA Laboratory was not accredited by the American Society of Crime Laboratory Directors at the time most of the samples in this case were tested. (Def. Mot. 35-36). To the extent that these and other passing arguments made in the Defendant's motion have not already been addressed earlier in this Memorandum Opinion, the Court concludes that these points impact only the weight of the evidence and are not bases for suppression.

CONCLUSION

For the foregoing reasons, Defendant's Motion To Exclude DNA Test Results and Request for *Daubert* Hearing will be denied by separate Order.

Date: March 16, 2009

_____/s/
ROGER W. TITUS
UNITED STATES DISTRICT JUDGE